

## Variable Heavy

A4.6.1      EIQLVQSGPELKQPGETVRISCKASGYTETNYGMNWVKQAPGKGLKWMG  
                  \*   \*   \* \* \*   \* \* \* \*   \*   \* \*  
 F(ab)-12   EVQLVESGGGLVQPGGSLRLSCAASGYTETNYGMNWVRQAPGKGLEWVG  
                  \*   \* \* \* \*   \*  
 humIII      EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVS  
                  1            10            20            30            40

A4.6.1      WINTYTGEPTYAADEFKRRFTFSLETSASTAYLQISNLKNDDTATYFCAK  
                  \*   \*   \* \* \* \*   \* \*  
 F(ab)-12   WINTYTGEPTYAADEFKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAK  
                  \*   \* \* \* \*   \* \* \* \*   \*  
 humIII      VISGDGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR  
                  50   a            60            70            80   abc            90

Fig. 1A

A4.6.1      YPHYYGSSHWFYFDVWGAGTTVTVSS (SEQ ID NO: 9)  
                  \*   \*  
 F(ab)-12   YPHYYGSSHWFYFDVWGQGT LVT VSS (SEQ ID NO: 7)  
                  \*   \*  
 humIII      G-----FDYWGQGT LVT VSS (SEQ ID NO: 11)  
                  110

## Variable Light

A4.6.1      DIQMTQTSSLSASLGDRVIISCSASODISNYLNWYQQKPDGTVKVLII  
                  \* \*   \*   \* \*   \* \* \* \*  
 F(ab)-12   DIQMTQSPSSLSASVGRVTITCSASODISNYLNWYQQKPGKAPKVLII  
                  \*   \*   \*   \*  
 humKI      DIQMTQSPSSLSASVGRVTITCRASQSI SNYLA WYQQKPGKAPKLLII  
                  1            10            20            30            40

Fig. 1B

A4.6.1      FTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCOOYSTVPWTF  
                  \* \*   \*   \*   \*  
 F(ab)-12   FTSSLHSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCOOYSTVPWTF  
                  \* \*   \*   \*  
 humKI      AASSLESGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQOYNSLPWTF  
                  50            60            70            80            90

A4.6.1      GGGTKLEIKR (SEQ ID NO: 10)  
                  \*   \*  
 F(ab)-12   GQGTKVEIKR (SEQ ID NO: 8)  
 humKI      GQGTKVEIKR (SEQ ID NO: 12)  
                  100

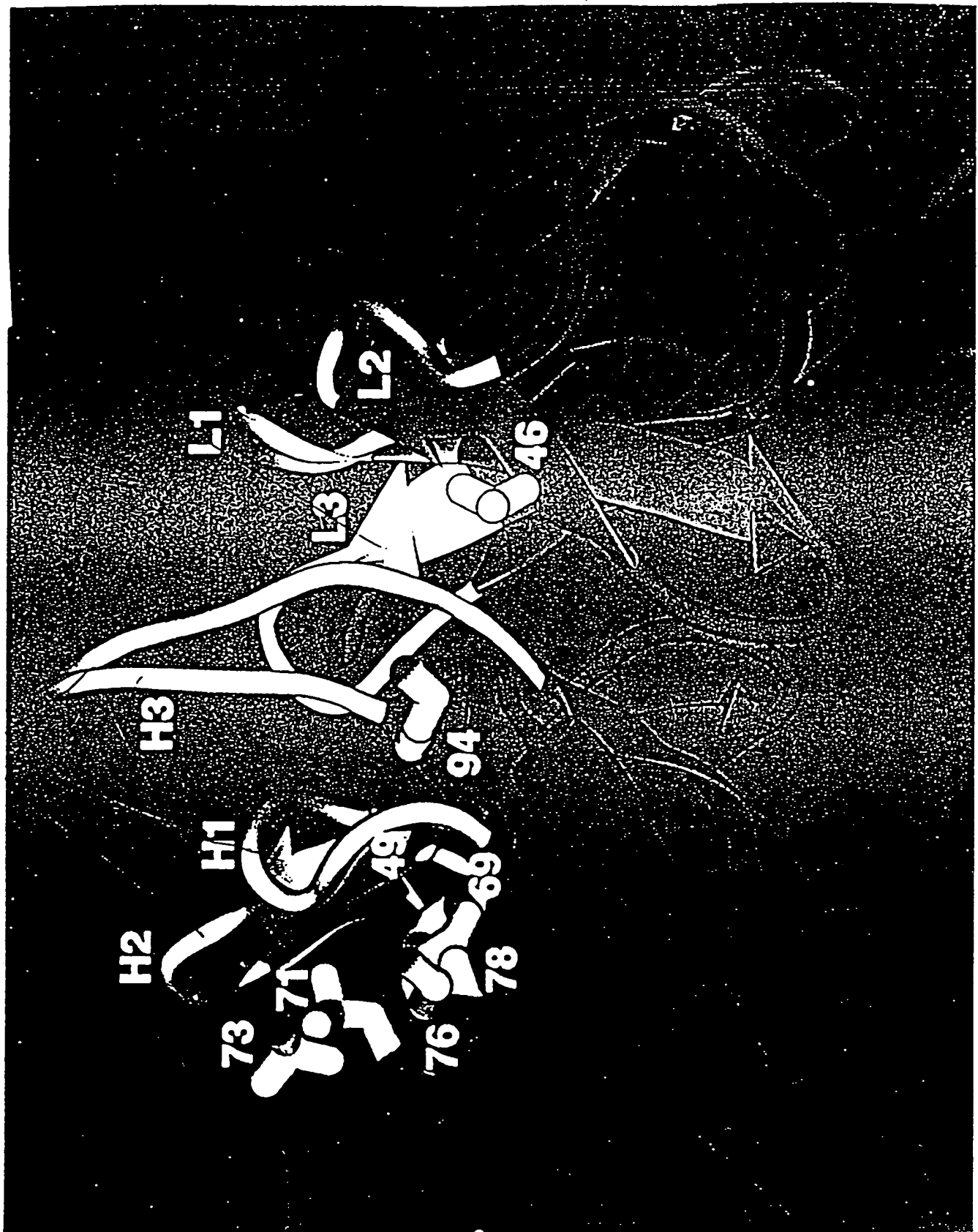


Fig. 2

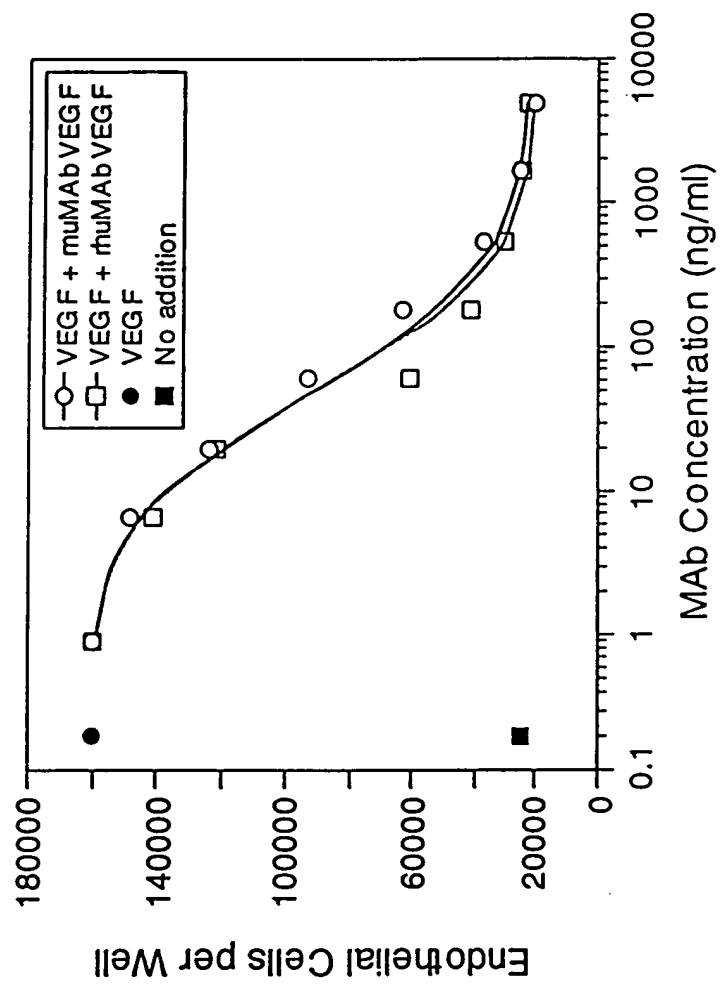
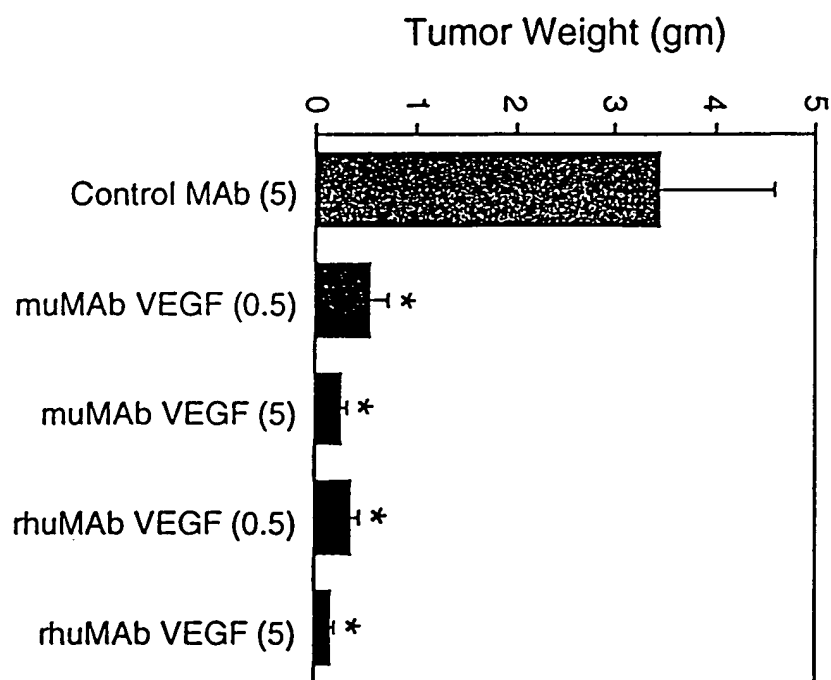


Fig. 3



**Fig. 4**

# V<sub>L</sub> domain

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          10          20          30          40
A4.6.1  DIQMTQTTSSLASLGDRVIISCSASQDISNYLNWYQQKP
          **          *          *
hu2.0   DIQMTQSPSSLSASVGDRVITITCSASQDISNYLNWYQQKP
hu2.10  DIQMTQSPSSLSASVGDRVITITCSASQDISNYLNWYQQKP

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Fig. 5A

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          50          60          70          80
A4.6.1  DGTVKVLIYFTSSLHSGVPSRFSGSGSGTDYSLTISNLEP
          **** *          **          *
hu2.0   GKAPKLLIYFTSSLHSGVPSRFSGSGSGTDFTLTISLQP
          .
hu2.10  GKAPKLLIYFTSSLHSGVPSRFSGSGSGTDYTLTISLQP

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          90          100
A4.6.1  EDIATYYCQOYSTVPWTFGGGKLEIK (SEQ ID NO:10)
          *          *
hu2.0   EDFATYYCQOYSTVPWTFGQGTKVEIK (SEQ ID NO:13)
hu2.10  EDFATYYCQOYSTVPWTFGQGTKVEIK (SEQ ID NO:15)

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# - V<sub>H</sub> domain

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          10          20          30          40
A4.6.1  EIQLVQSGPELKQPGETVRISCKASGYTFTNYGMNWVKQA
          * * ** * ** *
hu2.0   EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQA
          .
hu2.10  EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWIRQA

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Fig. 5B

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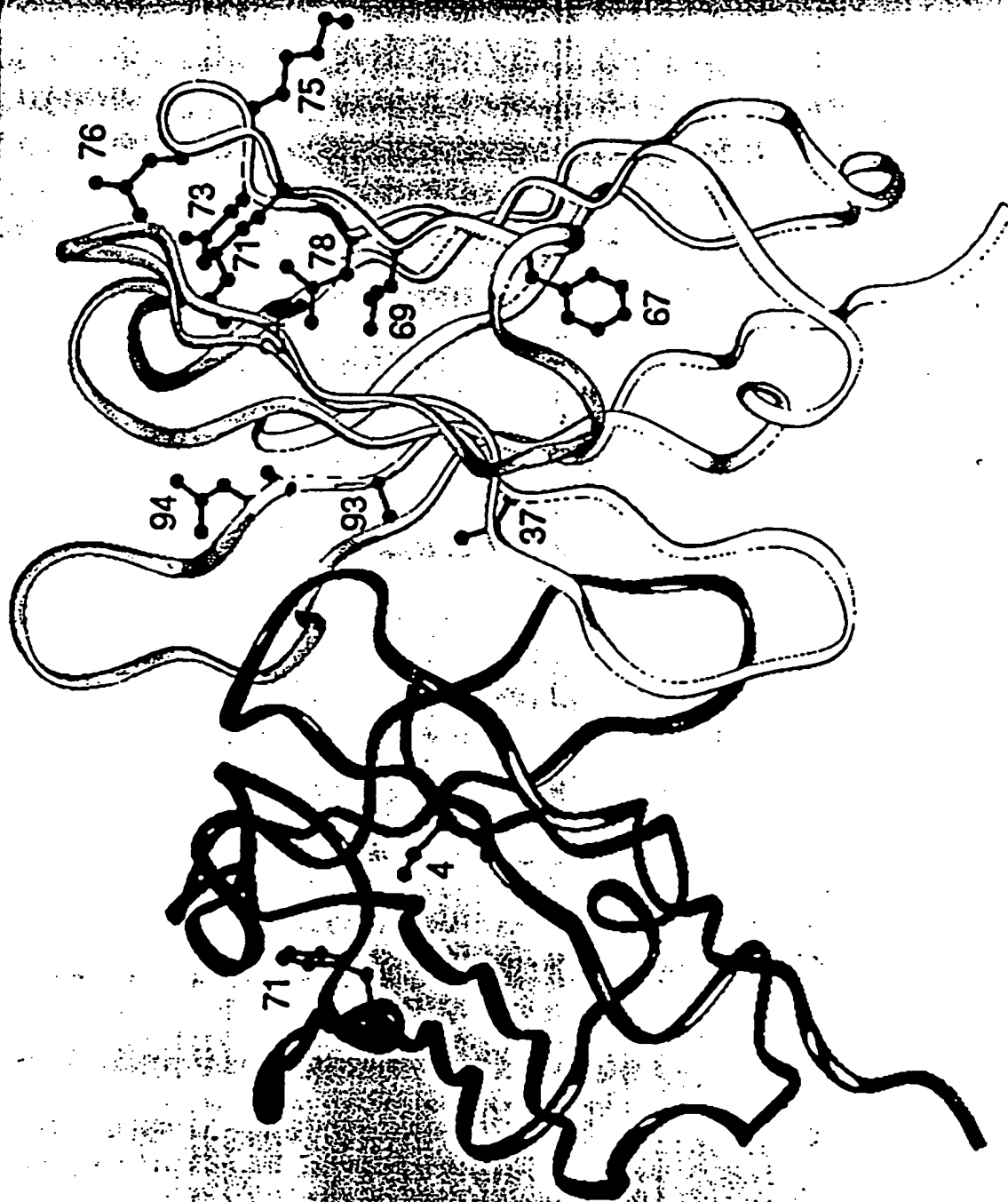
          50 a          60          70          80
A4.6.1  PGKGLKWMGWINTYTGEPTYAADFKRRFTFSLETSASTAYL
          * *          * ** *
hu2.0   PGKGLEWVGWINTYTGEPTYAADFKRRFTISRDNKNTLYL
          . . . .
hu2.10  PGKGLEWVGWINTYTGEPTYAADFKRRFTISLDTSASTVYL

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          abc          90          100abcdef          110
A4.6.1  QISNLKNDTATYFCAKYPHYYGSSHWYFDVWGAGTTVTVSS (SEQ ID NO:9)
          *** ** *
hu2.0   QMNSLRAEDTAVYYCARYPHYYGSSHWYFDVWGQGLVTVSS (SEQ ID NO:14)
          .
hu2.10  QMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGLVTVSS (SEQ ID NO:16)

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**Fig. 6**

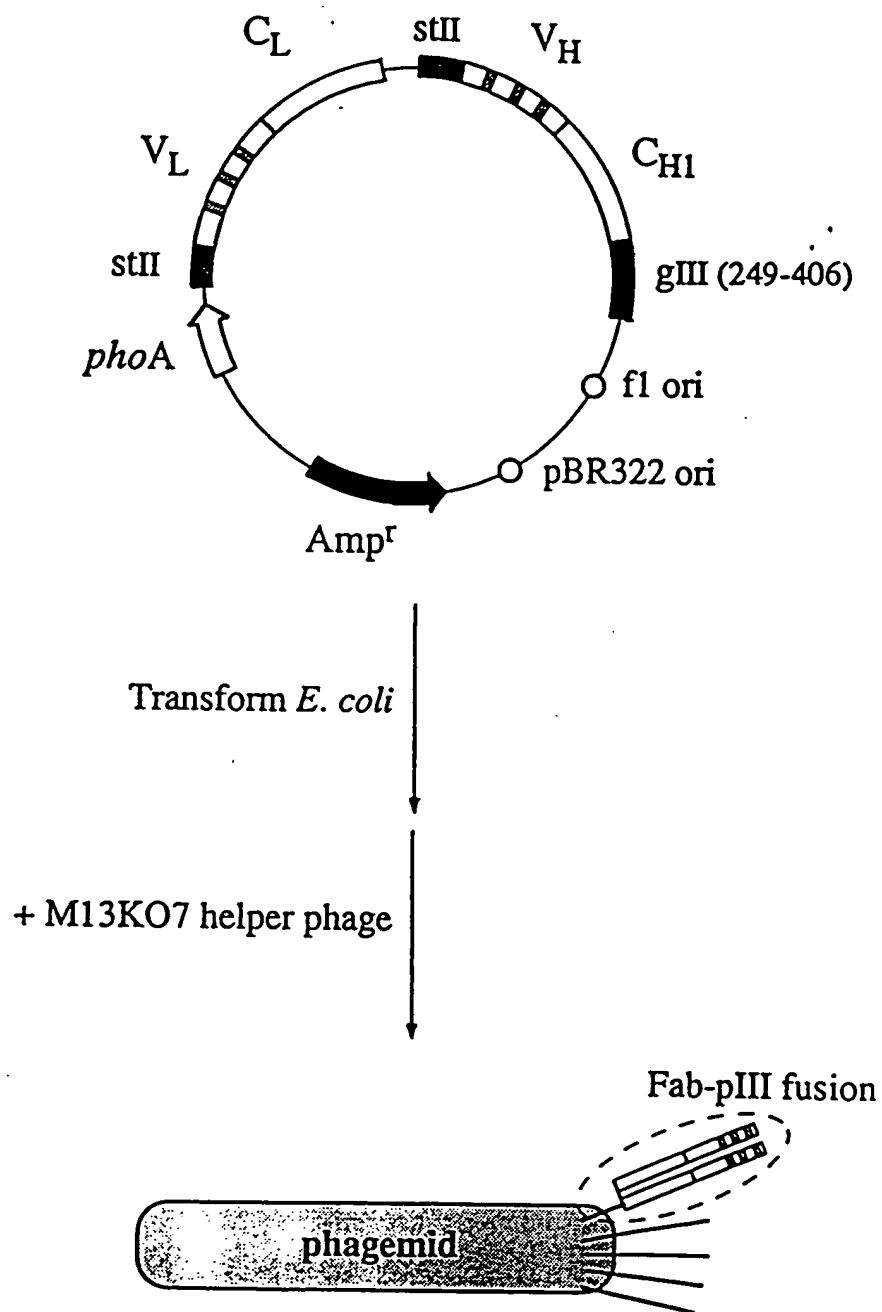


Fig. 7

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTAT AAGCTTTTGA GATTATCGTC ACTGCAATGC  
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTGTAG AGTAACGACT CAACAATAAA TTCGAAACCT CTAATAGCAG TGACGTTACG

101 TTGCAATAT GCGCAAAAT GACCAACAGC GGTGATTGA TCAGGTAGAG GGGCGCTGT ACGAGGTAA GCGCGATGCC AGCATTCCTG ACGACGATAC  
AAGCGTTATA CCGCGTTTGA CTGGTTGTGC CCAACTAACT AGTCCATCTC CCCCGGACA TGCTCCATTT CCGGCTACGG TCGTAAGGAC TGCTGCTATG

201 GGAGCTGCTG CCGGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT AAAAAGTTAA TCTTTTCAAC AGCTGTCTATA AAGTTGTAC GCGCGAGACT  
CCTCGACGAC GCGCTAATGC ATTTCTTCAA TAACTTCGTA GGAGCAGTCA TTTTTCATTT AGAAAAGTTG TCGACAGTAT TTCAACAGTG CCGGCTCTGA

301 TATAGTCGCT TTGTTTTTAT TTTTAAATGT ATTTGTAAT AGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGGTTGA GGTGATTTTA TGA AAAAAGAA  
ATATCAGCGA AACAAAAATA AAAAATTACA TAAACATTGA TCTTAAGCTC GAGCCATGGG CCCCTAGGAG ATCTCCAAT CCACATAAAT ACTTTTCTT  
-23 M etLysLysAsn  
Begin still signal sequence

401 TATCGCATTT CTTCTTGCAT CTATGTTTCGT TTTTCTTATT GCTACAAACG CGTACGCTGA TATCCAGTTG ACCAGTCCC CGAGCTCCCT GTCCGCTCT  
ATAGCGTAAA GAAGAACGTA GATACAAGCA AAAAAGATAA CGATGTTTGC GCATGCGACT ATAGGTCAAC TGGGTACGG GCTCGAGGGA CAGGCGGAGA  
-19 IleAlaPhe LeuLeuAlaSer erMetPheVa lPheSerIle AlaThrAsnA laTyrAlaAs pileGlnLeu ThrGlnSerP roSerSerLe uSerAlaSer  
Begin light chain

501 GTGGGGGATA GGTTCACCAT CACCTGCAGC GCAAGTCAGG ATATTAGCAA CTATTAAAC TGGTATCAAC AGAAACCAGG AAAAGCTCCG AAACACTACTGA  
CACCCGCTAT CCCAGTGGTA GTGGACGTCG CGTTCAGTCC TATAATCGTT GATAAATTTG ACCATAGTTG TCTTTGGTCC TTTTCGAGGC TTTGATGACT  
15 ValGlyAspA rGValThrII eThrCysSer AlaSerGlnA spIleSerAs nTyrLeuAsn TrpTyrGlnG InLysProG lYLysAlaPro LysLeuLeuIle

601 TTTACTTCAC CTCCTCTCTC CACTCTGGAG TCCCTTCTCG CTCTCTCTGA TCCGGTTCG GGACGGATTA CACTCTGACC ATCAGCAGTC TGCAGCCAGA  
AAATGAAGTG GAGGAGAGAG GTGAGACCTC AGGAAGAGC GAAGAGACCT AGGCAAGAC CTGCTCTAAT GTGAGACTGG TAGTCGTACG ACGTCGGTCT  
49 TyrPheTh rSerSerLeu HisSerGlyV alProSerAr gPheSerGly SerGlySerG lyThrAspTy rThrLeuThr ileSerSerL euGlnProGlu

701 AGACTTCGCA ACTTATTACT GTCAACAGTA TAGCACCGTG CCGTGGACGT TTGGACAGGG TACCAAGGTG GAGATCAAAAC GAACTGTGGC TGCACCATCT  
TCTGAAGCGT TGAATAATGA CAGTTGTCAT ATCGTGGCAC GGCACCTGCA AACCTGTCCC ATGGTTCCAC CTCTAGTTTG CTTGACACCG ACGTGGTAGA  
82 AspPheAla ThrTyrTyrC ysGlnGlnTy rSerThrVal ProTrpThrP heGlyGlnG lYThrLysVal GluIleLysA rGThrValAl aAlaProSer

801 GTCTTCATCT TCCGCCCATC TGATGAGCAG TTGAAATCTG GAACTGCTTC TGTTGTGTGC CTGCTGAATA ACTTCTATCC CAGAGAGGCC AAAGTACAGT  
CAGAAGTAGA AGGCGGTAG ACTACTCGTC AACTTTAGAC CTTGACGAAG ACAACACACG GACCACTTAT TGAAGATAGG GTCTCTCCGG TTTCATGTCA  
115 ValPheIleP heProProSe rAspGluGln LeuLysSerG lyThrAlase rValValCys LeuLeuAsnA snPheTyrPr oArgGluAla LysValGlnTrp

901 GGAAGGTGGA TAACGCCCTC CAATCGGGTA ACTCCCAGGA GAGTGTACAC GAGCAGGACA GCAAGGACAG CACCTACAGC CTCAGCAGCA CCCTGACGCT  
CCTTCCACCT ATTGCGGGAG GTTAGCCCAT TGAGGCTCCT CTCACAGTGT CTCGTCTGTG CGTTCCTGTC GTGGATGTGC GAGTCGTCTG GGGACTGCGA  
149 LysValas pAsnAlaLeu GlnSerGlyA snSerGlnG lUserValThr GluGlnAsps erLysAspse rThrTyrSer LeuSerSerL euSerThrLeu

1001 GAGCAAGACA GACTACGAGA AACACAAAGT CTACGCCCTG GAAGTCACCC ATCAGGGCCT GAGCTCGCC GTCACAAAGA GCTTCAACAG GGGAGAGTGT  
CTCGTTTCGT CTGATGCTCT TTGTGTTTCA GATGCGGACG CTTAGTGGG TAGTCCCGGA CTCGAGCGGG CAGTGTCTCT CGAAGTTGTC CCCTCTCACA  
182 SerLysAla AspTyrGluL ysHisLysVa lTyrAlaCys GluValThrH isGlnGlyLe uSerSerPro valThrLysS erPheAsnAr gGlyGluCys

Fig. 8A



1101 TAAGCTGATC CTCTACGCCG GACGCATCGT GGCCTTAGTA. GGAACTAGT GGTAAAGG GATCTAGAG GTTGAGGTGA TTTTATGAAA AAGAATATCG  
ATTGACTAG GAGATCGGC CTGCGTAGCA CCGGATCAT CGGTTGATCA GCATTTTCC CATAGATCTC CAACCTCCACT  
215 OC\* -23 MetLys LysAsnIleAla

1201 CATTTCTTCT TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGGGTAC GCTGAGGTTT AGCTGGTGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG  
GTAAAGAAGA ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGGCGCATG CGACTCCAAG TCGACCACCT CAGACCGCCA CCGGACCACG TCGGTCCCCC  
-17 PheLeuLe uAlaSerMet PheValPheS erIleAlaTh rAsnAlaTyr AlaGluValG lnLeuValGln uSerGlyGly GlyLeuValG lnProGlyGly

1301 CTCACCTCCGT TTGTCTCTGT CAGCTTCTGG CTATACCTTC ACCAACTATG GTATGAACCTG GATCCGCTAC GCCCGGGTA AGGCCCTGGA ATGGGTTGGA  
GAGTGAGGCA AACAGGACAC GTCGAAGACC GATATGGAAG TGGTTGATAC CATACTTGAC CTAGGCAGTC CGGGGCCCAT TCCCGGACCT TACCCAACCT  
17 SerLeuArg LeuSerCysA laAlaSerG1 yTyrThrPhe ThrAsnTyrG lyMetAsnTr pileArgGln AlaProGlyL yGlyLeuG1 uTrpValGly

1401 TGGATTAAACA CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG TCCTTTTACT ATATCTGCAG ACACCTCCAG CAACACAGTT TACCTGCAGA  
ACCTAATTGT GGATATGGCC ACTTGGCTGG ATACGACGCC TAAAGTTTGC AGCAAAATGA TATAGACGTC TGTGGAGGTC GTTGTGTCAA ATGGACGTCT  
50 TrpIleAsnT hrTyrThrG1 yGluProThr TyrAlaAlaA spPheLysAr gArgPheThr ileSerAlaA spThrSerSe rAsnThrVal TyrLeuGlnMet

1501 TGAACAGCCT GCGGCTGAG GACACTGCCG TCTATTACTG TGCAAGTAC CCGCACTATT ATGGGAGCAG CCACCTGGTAT TTCGACGTCT GGGGTCAAGG  
ACTGTCCGA CGCGGACTC CTGTGACGGC AGATAATGAC ACGTTTCATG GCGTGATAA TACCCTCGTC GGTGACCATA AAGCTGCAGA CCCAGTTCC  
84 AsnSerLe uArgAlaGlu AspThrAlav alTyrTyrCy salalLysTyr ProHisTyrT yrglyserSe rHisTrpTyr PheAspValT rpGlyGlnGly

1601 AACCCCTGGT ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGGC  
TTGGGACCAG TGGCAGAGGA GCCGGAGGTG GTTCCCGGT AGCCAGAGG GGGACCGTGG GAGGAGTTC TCGTGGAGAC CCCCCTGTGC CCGGACCCCG  
117 ThrLeuVal ThrValSers erAlaSerTh rLysGlyPro SerValPheP roLeuAlaPr oSerSerLys SerThrSerg lyGlyThrAl aAlaLeuGly

1701 TGCCTGGTCA AGGACTACTT CCCGAAACCG GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC CTACAGTCTT  
ACGGACCAGT TCCTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG TCCGCGGAC TGGTGGCGC ACGTGTGGAA GGGCCGACAG GATGTGAGA  
150 CysLeuValL yAspTyrPh eProGluPro valThrValS ertTrpAsnSe rGlyAlaLeu ThrSerGlyV alHisThrPh eProAlaVal LeuGlnSerSer

1801 CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA  
GTCTTGAGAT GAGGAGTGC TCGCACCACT GGCACGGGAG GTCGTGGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTTCGGT CGTTGTGGT  
184 GlyLeuTy rSerLeuSer SerValValt hrValProse rSerSerLeu GlyThrGlnT hrTyrIleCy sAsnValAsn HisLysProS erAsnThrLys

1901 GGTGACAAAG AAAGTTGAGC CCAAATCTTG TGACAAAACCT CACCTCTAGA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAA  
CCAGCTGTTT TTTCAACTCG GGTTAGAAC ACTGTTTGA GTGGAGATCT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG  
217 ValAspLys LysValGluP roLysSerCy sasplLysThr HisLeuAM\*S erGlyGlyG1 ySerGlySer GlyAspPhea spTyrGluLy sMetAlaAsn

2001 GCTAATAAGG GGGCTATGAC CGAAAATGCC GATGAAAACG CGTACAGTC TGACGCTAAA GGCAAACTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA  
CGATTATTCC CCCGATACTG CTTTTTACGG CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT  
250 AlaAsnLysG lyAlaMetTh rGluAsnAla AspGluAsnA laLeuGlnSe rAspAlaLys GlyLysLeuA spSerValAl aThrAspTyr GlyAlaAlaIle

2101 TCGATGGTTT CATTGGTGAC GTTTCGGGCC TTGCTAATGG TAATGGTGCT ACTGGTGATT TTGCTGGCTC TAATTCCTCA ATGGCTCAAG TCGGTGACGG  
AGCTACCAA GTAACCACTG CAAAGGCCGG AACGATTACC ATTACCACGA TGACCACCTAA AACGACCGAG ATTAAGGCTT TACCGAGTTC AGCCACTGCC  
284 AspGlyPh eIleGlyAsp ValSerGlyL euAlaAsnG1 yAsnGlyAla ThrGlyAspP heAlaGlySe rAsnSerGln MetAlaGlnV alGlyAspGly

2201 TGATAATTCA CCTTAAATGA ATAATTTCCG TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTCGC CTTTTGTCT TTAGCGCTGG TAAACCATAT  
ACTATTAAAGT GAAATTACT TATTAAAGC AGTTATAAAT GAGTAGCCA ACTTACAGCG GGAACACAGA AATCGGACC ATTTGGTATA  
317 AspAsnSer ProLeuMeta sAsnPhear gGlnTyrLeu ProSerLeup roGlnSerVa lGluCysArg PropheValP heSerAlaG1 yLysProTyr

Fig. 8B

2301 GAATTTTCTA TTGATTGTGA CAAATAAAGC TTATTGGCTG GTGCTTTTGG GTTCTGTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA  
 CTTAAAAGAT AACTAACACT GTTTTATTGG AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAATAACAT ACATAAAAGA TGCAAAACGAT  
 350 GluPheSerI leAspCysAs pLysIleAsn LeuPheArg lyValPheAl apHeLeuLeu TyrValAlaIat hrPheMetty rValPheSer ThrPheAlaAsn  
 2401 ACATACTGGG TAATAAGGAG TCTTAATCAT GCCAGTTCTT TTGGCTAGCG CCGCCCTATA CCTTGCTGCG CTCCCCCGGT TGCGTCGCGG TGCATGGAGC  
 TGTATGACGC ATTATTCCTC AGAATTAGPA CGGTCAAGAA AACCGATCGC GCGGGGATAT GGAACAGACG GAGGGGCGCA ACGCAGCGCC ACGTACCTCG  
 384 IleLeuAr gasnLysGlu SerOC\* (SEQ ID NO: 100)  
 end g3 protein  
 2501 CGGGCCACCT CGACCTGAAT GGAAGCCGGC GGCACCTCGC TAACGGATTG ACCACTCCAA GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC  
 GCGCGGTGGA GCTGGACTTA CCTTCGGCGG CCGTGGAGCG ATTGCCTAAG TGGTAGGTT CTTAACCTCG GTTAGTTAAG AACGCCTCTT GACACTTACG  
 2601 GCAAAACCAAC CCTTGGCAGA ACATATCCAT CGCGTCCGCC ATCTCCAGCA GCGGCACGCG GCGCATCTCG GGCAGCGTTG GGTCTGGCC ACGGGTGCGC  
 CGTTTGGTTG GGAACCGTCT TGTATAGGTA GCGCAGCGCG TAGAGTCTGT CCGCGTGGC GCGCTAGAGC CCGTCGCAAC CCAGGACCGG TGCCACGCG  
 2701 ATGATCGTGC TCCTGTCTGT GAGGACCCCG CTAGGCTGGC GGGTTGCCCT TACTGGTTAG CAGAATGAAT CACCGAATAC GTGGCTATGC GCTCGCTTGC ACTTCGCTGA  
 TACTAGCACG AGGACAGCAA CTCCTGGGCC GATCCGACCG CCCCACGGA ATGACCAATC GTCTTACTTA GTGGCTATGC GCTCGCTTGC ACTTCGCTGA  
 2801 GCTGCTGCAA AACGCTGCG ACCTGAGCAA CAACATGAAT GGTCTTCGGT TTCCGTCGTT CGTAAAGTCT GGAACGCGG AAGTCAGCGC CCGTCACCAT  
 CGACGACGTT TTGCAGACGC TGGACTCGTT GTTGTACTTA CCAGNAGCCA AAGGCACAAA GCATTTTCAGA CCTTTGCGCC TTCAGTCGCG GGACGTGGTA  
 2901 TATGTTCCGG ATCTGCATCG CAGGATGCTG CTGGCTACCC TGTGGAACAC CTACATCTGT ATTAACGAAG CGCTGGCATT GACCCCTGAGT GATTTTTCTC  
 ATACAAGGCC TAGACGTAGC GTCTCTACGAC GACCGATGGG ACACCTTGTG GATGTAGACA TAATTGCTTC GCGACCGTAA CTTGGGACTCA CTAAAAAGAG  
 3001 TGGTCCCGCC GCATCCATAC CGCCAGTTGT TTACCCTCAC AACGTTCCAG TAACCGGGCA TGTTTCATCAT CAGTAACCCG TATCGTGAGC ATCCTCTCTC  
 ACCAGGGCGG CGTAGGTATG GCGGTCAACA AATGGGAGTG TTGCAAGGTC ATTGGCCCGT ACAAGTAGTA GTCATTTGGC ATAGCACTCG TAGGAGAGAG  
 3101 GTTTCATCGG TATCATTAAC CCCATGAACA GAATTTCCCC CTTACACGGA GGCATCAAGT GACCAAAACAG GAATAAACCG CCCTTAAACAT GGCCCGCTTT  
 CAAAGTAGCC ATAGTAATGG GGTACTTGT CTTTAAGGGG GAATGTGCTC CCGTAGTTCA CTGTTTGTG CTTTCTTGGC GGGAAATTGA CCGGGCGAAA  
 3201 ATCAGAAGCC AGACATTAAC GCTTCTGGAG AAACCTCAACG AGCTGGACGC GGATGAACAG GCAGACATCT GTGAATCGCT TCACGACCAC GCTGATGAGC  
 TAGTCTTCGG TCTGTAATTG CGAAGACCTC TTTGAGTTGC TCGACCTGCG CCTACTTGTC CGTCTGTAGA CACTTAGCGA AGTGTGCTG CGACTACTCG  
 3301 TTTACCGCAG GATCCGGAAA TTGTAAACGT TAATATTTTG TTAAAATTG CGTTAAATTT TGTFTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC  
 AAATGGCGTC CTAGGCCCTT CTAGGCCCTT AACATTGCA ATTATAAAC AATTTAAGC GCAATTTAA AACAATTTAG TCGAGTAAAA AATTGGTTAT CCGGCTTTAG  
 3401 GGCAAAATCC CTTATAAATC AAAAGAATAG ACCGAGATAG GGTGAGTGT TGTTCAGTT TGGAAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG  
 CCGTTTTAGG GAATATTTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA ACCTTGTTCT CAGGTGATAA TTTCTTTGCAC CTGAGGTTGC  
 3501 TCAAAGGGCG AAAAACCGTC TATCAGGGCT ATGGCCCACT ACGTGAACCA TCACCTTAAT CAAAGTTTTT GGGGTGAGG TGCCGTAAAG CACTAAATCG  
 AGTTTCCCGC TTTTGGCAG ATAGTCCCGA TACCGGGTGA TGCATTGGT AGTGGGATTA GTTCAAAAAA CCCCAGCTCC ACGGCATTC GTGATTAGC  
 3601 GAACCCCTAA GGGAGCCCC GATTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGAAAGG AAGGAGCGG CGCTAGGGCG  
 CTTGGGATTT CCCTCGGGG CTAAATCTCG AACTGCCCTT TCGGCCGCT TGCACCGCTC TTCTTTCCGT TTCCTCGCC GCGATCCCGC  
 3701 CTGGCAAGTG TAGCGGTAC GCTGCGCGTA ACCACACAC CCGCCGCGCT TAATGCGCG CTACAGGGCG CGTCCGGATC CTGCCCTCGG CGTTTCGGTG  
 GACCGTTTAC ATGCCAGTG CGACGGCAT TGGTGGTGTG GCGCGCGGA ATTACGCGG GATGTCCCG CAGGCGCTAG GACGGAGCGC GCAAAGCCAC  
 3801 ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC GGTACAGCT TGTCTGTAAG CCGATGCCG GAGCAGACAA GCCGTGAGG GCGGTGAGC  
 TACTGCCACT TTTGGAGACT GTGTACGTG AGGCCCTCTG AGGCCCTCTG CCAGTGTGCA ACAGACATTC GCTTACGGC CTCGTCTGTT CCGGCAGTCC GCGCAGTCC

Fig. 8C

3901 GGGTGTGGC GGGGTGCGG GGCAGCCAT GACCCAGTCA CGTAGCGATA GGGAGTGTA TACTGGCTTA ACTATGCGG ATCAGAGCAG ATTGTACTGA  
CCCACAAACG CCCACAGCCC CGCGTCGGTA CTGGGTCACT CGCTCACAT ATGACCGAAT TGATACGCCG TAGTCTCGT TAACATGACT  
4001 GAGTGCACCA TATCGGGTGT GAAATACCG ACAGATGCGT AAGGAGAAAA TACCGCATCA GCGCTCTTC CGCTTCTCG CTCACTGACT CGCTGCGCTC  
CTCACGTGGT ATACGCCACA CTTTATGGCG TGTCTACGCA TTCCTCTTTT ATGGCGTAGT CCGGAGAAAG GCGAAGGAGC GAGTGACTGA GCGACGCGAG  
4101 GGTGCTTCGG CTGCGGCGAG CGGTATCAGC TCACCTCAAAG GCGGTAATAC GGTATCCAC AGAATCAGG GATAACGAG GAAAGAACAT GTGAGCAAAA  
CCAGCAAGCC GACGCCGCTC GCCATAGTCG AGTGAGTTT CGCCATTATG CCAATAGGTG TCTTAGTCCC CTATTGCGTC CTTTCTTGTA CACTCGTTTTT  
4201 GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCGCGTTGC TGGCGTTTTT CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAAATCGA CGCTCAAGTC  
CCGGTCGTTT TCCGGTCCTT GGCATTTTTC CCGCGCAACG ACCGCAAAA GGTATCCGAG GCGGGGGAC TGCTCGTAGT GTTTTTAGCT GCGAGTTTACG  
4301 AGAGGTGGC AAACCCGACA GGAATATAA GATACAGGC GTTCCCCCT GGAAGCTCCC TCGTGGCTC TCCTGTTCG ACCCTGCCG TTACCGGATA  
TCTCCACCGC TTGGGCTGT CCTGATATT CTATGGTCCG CAAAGGGGA CCTTCAGGG AGCACAGGC AGGACAGGC TGGGACGGC AATGGCCTAT  
4401 CCTGTCCGCC TTTCTCCCTT CGGGAAGCGT GCGCTTTCT CATAGCTCAC GCTGTAGGTA TCTCAGTTTC GTGTAGTTCG TTCTGCTCAA GCTGGGCTGT  
GGACAGGCGG AAAGAGGGAA GCCCTTCGCA CCGCGAAAGA GTATCGAGTG CGACATCCAT AGAGTCAAGC CACATCCAGC AAGCGAGGT CGACCCGACA  
4501 GTGCACGAAC CCCCCGTTCA GCGGACCGC TCGCCCTTAT CCGGTAACTA TCGTCTTGAG TCCAAACCGG TAAGACACGA CTTATCGCCA CTGGCAGCAG  
CACGTGCTTG GGGGCAAGT CCGGCTGGC AGCGGAATA GGCCATTGAT AGCAGAACTC AGGTGGGCC ATTCTGTGCT GAATAGCGGT GACCGTCGTC  
4601 CCACTGGTAA CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCTTAA CTACGGCTAC ACTAGAAGGA CAGTATTTGG  
GGTGACCAAT GTCTAATCG TCTCGTCCA TACATCCGCC AGATGTCTC AAGAACTTCA CCACCGGAT GATGCCGATG TGATCTTCT GTCATAAACC  
4701 TATCTGCGCT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA GTTGTAGCT CTGTATCCG CAAACAACC ACCGTGTA GCGGTGGTT TTTTGTGTC  
ATAGACGCGA GACGACTCG GTCAATGGAA GCCTTTTCT CAACCATCGA GAACTAGGCC GTTGTGTTGG TGGGACCAT CGCCACCAA AAAACAAACG  
4801 AAGCAGCAGA TTACGCGCAG AAAAAAGGA TCTCAAGAAG ATCCTTTGAT CTTTCTACG GGTCTGACG CTCAGTGGAA CGAAAACTCA CGTTAAGGGA  
TTCGTGCTCT AATGCGGCTC TTTTCTTCT AGAGTTCTTC TAGGAACTA GAAAAAGATC CCAGACTGC GAGTACCTT GCTTTTGTG GCAATTCCT  
4901 TTTTGGTCT GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC AATCTAAGT ATATATGAGT AAACCTGGTC  
AAAACCACTA CTCTAATAGT TTTTCTTCTA AGTGGATCTA AGTGGATCTA ATTTTACTT CAAAAATTTAG TTAGATTTC TATATACTCA TTTGAACACG  
5001 TGACAGTTAC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGC TATTTCTGTC ATCCATAGTT GCCTGACTCC CCGTCGCTGA GATAACTACG  
ACTGTCAATG GTTACGAAT AGTCACTCCG TGATAGAGT CGCTAGACAG ATAAAGCAAG TAGGTATCAA CGGACTGAG GGCAGCACAT CTATTGATGC  
5101 ATACGGGAGG GCTTACCATC TGGCCCCAGT TGGCCCCAGT GCTGCAATGA TACCGCGAGA CCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCCAG CCAGCCGGAA  
TATGCCCTCC CGAATGGTAG ACCGGGTCA CGACGTTACT ATGGCGCTCT GGGTGGAGT GGCCGAGGTC TAAATAGTCG TTATTTGGTC GGTGCGCTT  
5201 GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCTC CATCCAGTCT ATTAATTGTT GCCGGGAAGC TAGAGTAAGT AGTTGCCAG TTAATAGTTT  
CCCGGCTCGC GTCTTACCA GAGCTTGA GAGCTTGA ATAGGCGGAG GTAGGTCAGA TAATTAACAA CGGCCCTTCG ATCTCATTC TCAAGCGGTC AATTATCAA  
5301 GCGCAACGTT GTTGCCATTG CTGAGGCGAT CGTGTGTCA CGCTGCTCT GCGAGCAGCA AACCATACC AAGTAAGTCG AGGCCAAGG TTGCTAGTTC CGCTCAATGT  
CGCGTTGCAA CAACGGTAAC GACGTCCGTA GCACCACAGT GCAGCAGCTA GCAACAGTCT TCATTCAACC GCGCTCACA TAGTGAGTAC CAATACCGTC  
5401 TGATCCCCA TGTGTGCAA AAAAGCGGT AGCTCCTTCG GTCCCTCCGAT CGTTGTGAGA AGTAAGTTGG CCGCAGTGT ATCACTCATG GTTATGGCAG  
ACTAGGGGT ACAACAGCT TTTTCGCCA TCGAGGAAGC CAGGAGGCTA GCAACAGTCT TCATTCAACC GCGCTCACA TAGTGAGTAC CAATACCGTC  
5501 CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTGGTGTG ACTCAACCAA GTCATTTCTGA GAATAGTGA TGCGGCGACC  
GTGACGTAAT AAGAGATGA CAGTACGGTA GGCATTCTAC GAAAGACAC TGACCACCTCA TGAGTTGGTT CAGTAAGACT CTTATCACAT ACGCCGCTGG

Fig. 8D

5601 GAGTTGCTCT TGCCCGGCGT CAACACGGGA TAATA~~GGGG~~GGACATAGCA GAAC~~TTTT~~TANA AGT~~GT~~CTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC  
CTCAACGAGA ACGGGCCGCA GTTG~~TGCC~~CT TTATGGCGC GGTGTATCGT CTTGAAATTT TCACGAGTAG TAACCTTTTG CAAGAAGCCC CGCTTTTGAG

5701 TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG  
AGTTCCCTAGA ATGGCGACAA CTCTAGGTCA AGCTACATTG GGTGAGCAG GGGTTGACT AGAAGTCGTA GAAAATGAAA GTGTCGCAA AGACCCACTC

5801 CAAAAACAGG AAGGCAAAAT GCCGCAAAA AGGGAATAAG GCGACACAGG AAATGTTGAA TACTCATACT CTTCCTTTT CAATATTATT GAAGCATTTA  
GTTTTTGTCC TTCCGTTTTA CGCGTTTTT TCCCTTATTC CCGCTGTGCC TTTACAACTT ATGAGTATGA GAAGGAAAA GTTATAATAA CTTCGTAAAT

5901 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAA TAAATCTTTT TATTTGTTA TCCCCAAGGC GCGTGTAAAG GGGCTTTTCA CCGTGGACTG  
AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTACA TAAATCTTTT TATTTGTTA TCCCCAAGGC GCGTGTAAAG GGGCTTTTCA CCGTGGACTG

6001 GTCTAAGAAA CCATTATTAT CATGACATTA ACCTATAAAA ATAGGCGTAT CACGAGGCC TTTCGTCTTC AA (SEQ ID NO: 99)  
CAGATTCTTT GGTAATAATA GTACTGTAAT TGGATATTTT TATCCGCATA GTGCTCCGGG AAAGCAGAAG TT

Fig. 8E

■ = differences from F(ab)-12

		10	20	30
F(ab)-12	DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ			
MB1.6	DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ			
H2305.6	DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ			
Y0101	DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ			
Y0192	DIQ■TQSPSSLSASVGDRVTITC■RANFQ■SNYLNWYQQ			

		40	50	60	70
		CDR-L1			
F(ab)-12	KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS				
MB1.6	KPGKAPK■LIIYFTSSLHSGVPSRFSGSGSGTD■FTLTIS				
H2305.6	KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTD■FTLTIS				
Y0101	KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS				
Y0192	KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS				

Fig. 9A

		80	90	100
		CDR-L2		
F(ab)-12	SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 8)			
MB1.6	SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 101)			
H2305.6	SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 103)			
Y0101	SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 105)			
Y0192	SLQPEDFATYYCQQYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 107)			

CDR-L3

		10	20	30
F(ab)-12	EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR			
MB1.6	EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNW■R			
H2305.6	EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNW■R			
Y0101	EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR			
Y0192	EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYG■NWVR			

		40	50	60	70
		CDR-H1			
F(ab)-12	QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA				
MB1.6	QAPGKGLEWVGWINTYTGEPTYAADFKRRFT■SADTS■SNIV				
H2305.6	QAPGKGLEWVGWINTYTGEPTYAADFKRRFTF■SADTS■SNIV				
Y0101	QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA				
Y0192	QAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTA				

Fig. 9B

		80	90	100	110
		CDR-H2		CDR-7	
F(ab)-12	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGT (SEQ ID NO: 7)				
MB1.6	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGT (SEQ ID NO: 102)				
H2305.6	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGT (SEQ ID NO: 104)				
Y0101	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGT (SEQ ID NO: 106)				
Y0192	YLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGT (SEQ ID NO: 108)				

CDR-H3

■ = differences from )-12

10 20 30  
F(ab)-12 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ  
Y0243-1 DIQ■TQSPSSLSASVGDRVTITC■RANE■ISNYLNWYQQ  
Y0238-3 DIQ■TQSPSSLSASVGDRVTITC■RANE■ISNYLNWYQQ  
Y0313-1 DIQ■TQSPSSLSASVGDRVTITC■RANE■ISNYLNWYQQ  
Y0317 DIQ■TQSPSSLSASVGDRVTITCSASQDISNYLNWYQQ

CDR-L1

40 50 60 70  
F(ab)-12 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0243-1 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0238-3 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0313-1 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS  
Y0317 KPGKAPKVLIIYFTSSLHSGVPSRFSGSGSGTDFTLTIS

Fig. 10A

CDR-L2

80 90 100  
F(ab)-12 SLQPEDFATYYCQOYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 8)  
Y0243-1 SLQPEDFATYYCQOYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 109)  
Y0238-3 SLQPEDFATYYCQOYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 111)  
Y0313-1 SLQPEDFATYYCQOYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 113)  
Y0317 SLQPEDFATYYCQOYSTVPWTFGQGTKVEIKRTV (SEQ ID NO: 115)

CDR-L3

10 20 30  
F(ab)-12 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVR  
Y0243-1 EVQLVESGGGLVQPGGSLRLSCAASGY■FT■HYGMNWVR  
Y0238-3 EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYG■NWVR  
Y0313-1 EVQLVESGGGLVQPGGSLRLSCAASGY■FT■HYGMNWVR  
Y0317 EVQLVESGGGLVQPGGSLRLSCAASGY■FT■HYGMNWVR

CDR-H1

40 50 60 70  
F(ab)-12 QAPGKGLEWVGWINTYTGEPTYAADFRRFTFSLDTSKSTA  
Y0243-1 QAPGKGLEWVGWINTYTGEPTYAADFRRFTFSLDTSKSTA  
Y0238-3 QAPGKGLEWVGWINTYTGEPTYAADFRRFTFSLDTSKSTA  
Y0313-1 QAPGKGLEWVGWINTYTGEPTYAADFRRFTFSLDTSKSTA  
Y0317 QAPGKGLEWVGWINTYTGEPTYAADFRRFTFSLDTSKSTA

Fig. 10B

CDR-H2

80 90 100 110 CDR-7  
F(ab)-12 YLQMNSLRAEDTAVYYCAKYPHYGSSHWHYFDVWGQGT (SEQ ID NO: 7)  
Y0243-1 YLQMNSLRAEDTAVYYCAKYPHYGSSHWHYFDVWGQGT (SEQ ID NO: 110)  
Y0238-3 YLQMNSLRAEDTAVYYCAKYP■Y■G■SHWHYFDVWGQGT (SEQ ID NO: 112)  
Y0313-1 YLQMNSLRAEDTAVYYCAKYP■Y■G■SHWHYFDVWGQGT (SEQ ID NO: 114)  
Y0317 YLQMNSLRAEDTAVYYCAKYP■Y■G■SHWHYFDVWGQGT (SEQ ID NO: 116)

CDR-H3

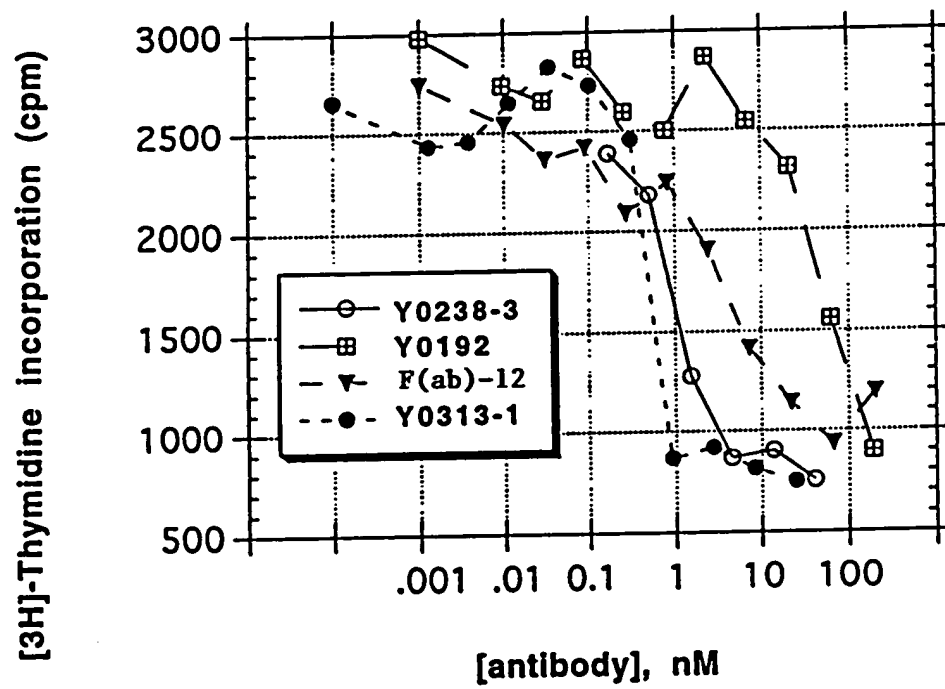


Fig. 11

Fig. 12

